



Mo5176new.txt

<110> Bayer Aktiengesellschaft

<120> Nucleic Acids which encode
insect acetylcholine receptor subunits

<130> Le A 33 020-Foreign Countries

<140> US/09/303,232

<141> 1999-04-30

<150> DE 198 19 829.9

<151> 1998-05-04

<160> 14

<170> PatentIn Ver. 2.1

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<213> Drosophila melanogaster

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<221> CDS

<222> (372)..(2681)

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aatttcgtaa gattagttgg tattaagggc agcccatgca cacagctaaa aagggaacta 240
aaaaaacccc gcacagaaca atgaaagctg cagcagctgg ataaggccga caaaaccgaa 300
aattatatta ttgtaatcta gtagagagca gacaacatat ccgctggcaa caaccaacac 360
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Asp Glu Leu Trp Leu Ala Val Arg Leu Ala His Cys Ser Ser Asn Phe
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Ser Ser Ser Ser Ser Thr Arg Thr Thr Ser Ser Asn Gln Arg His Asn
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cag caa ctc aca aca ctg caa cca agg agc tta agt aca aaa cac cac 554
Gln Gln Leu Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His
          50             55             60
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Ser Asn Ile Ala Ser Glu Gln His Asn Ser Gln Gln Gln Glu Pro Ala
          65             70             75
tcg aag gac gag gat gta gcc aac cac ggt aga agc aat gac cag cag 650
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Mo5176new.txt

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Ala Ala Ala Ala Thr 115 Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro 125	
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Thr Asn Ile Arg Leu 130 Cys Ala Arg Lys Arg 135 Gln Arg Leu Arg Arg 140 Arg Arg	
cga aaa aga aaa cca gca acc cca aac gaa aca gat atc aag aaa caa	842
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Gln Gln Leu 160 Ser Met Pro Pro Phe 165 Lys Thr Arg Lys Ser 170 Thr Asp Thr	
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Tyr Ser 175 Thr Pro Ala Ala Thr 180 Thr Ser Cys Pro Thr 185 Ala Thr Tyr Met	
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Gln Cys Arg Ala Ser 195 Asp Asn Glu Phe Ser Ile 200 Pro Ile Ser Arg His 205	
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Asp Arg Val Ser Thr 210 Ala Thr Phe Ala Trp Val Leu His Val Leu Gln 220	
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Val Leu Leu Val 225 Ser Leu Gln Gln Trp 230 Gln Leu His Val Gln Gln Arg 235	
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Ser Val Leu 240 Leu Phe Arg Arg Ile 245 Ala Ala Ser Thr Ile 250 Ala Phe Ile	
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Ser Tyr 255 Leu Gly Ser Phe 260 Ala Ala Gln Leu Lys Asn 265 Ser Ser Ser Ser	
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Ser Ser Ser Ser Asn 275 Ser Ser Asn Asn Ser 280 Thr Gln Ile Leu Asn 285	
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Gly Leu Asn Lys 290 His Ser Trp Ile Phe Leu 295 Leu Leu Ile Tyr Leu Asn Leu 300	
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Asp Leu Leu 320 Asp Pro Tyr Asn Thr 325 Leu Glu Arg Pro Val Leu Asn Glu 330	
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Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile	

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370	Leu Glu Trp Asn Asp Met Asn Leu Arg Trp Asn Thr Ser Asp Tyr Gly	380
385	gga gtt aag gat ctg cga ata ccg ccg cat cgc atc tgg aag ccg gac	1562
390	Gly Val Lys Asp Leu Arg Ile Pro Pro His Arg Ile Trp Lys Pro Asp	395
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405	Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe Asp Gly Thr Tyr Gln	410
415	acg aac gtg gtg gtg cgg aac aac ggc tcg tgt cta tac gtt ccg ccg	1658
420	Thr Asn Val Val Val Arg Asn Asn Gly Ser Cys Leu Tyr Val Pro Pro	425
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435	Gly Ile Phe Lys Ser Thr Cys Lys Ile Asp Ile Thr Trp Phe Pro Phe	440
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495	cgt aac gag atc tat tac aac tgc tgc ccg gaa ccc tat ata gac atc	1898
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570	gct act tcc gat gcg gtg cca ttg tgg ata cgc atc gtg ttt ttg tgc	2138
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Mo5176new.txt

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 Ala Ser Glu Gln His Asn Ser Gln Gln Gln Glu Pro Ala Ser Lys Asp
 65 70 75 80
 Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln Thr His Leu
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 Gln Gln Leu Asp Ser Ser Asn Met Leu Ser Pro Lys Thr Ala Ala Ala
 100 105 110
 Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro Thr Asn Ile
 115 120 125
 Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg Arg Lys Arg
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 Lys Pro Ala Thr Pro Asn Glu Thr Asp Ile Lys Lys Gln Gln Gln Leu
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 Ala Ser Asp Asn Glu Phe Ser Ile Pro Ile Ser Arg His Asp Arg Val
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 645 650 655
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 675 680 685

Mo5176new.txt

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 Ser His Leu Ala Ala Pro Ala Gly Leu Leu Leu Leu Leu Cys Leu Leu
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 Trp Pro Arg Gly Ala Arg Cys Gly Tyr His Glu Lys Arg Leu Leu His
 25 30 35
 cac cta ttg gac cac tac aac gta ctg gag agg ccc gtc gtc aac gag 499
 His Leu Leu Asp His Tyr Asn Val Leu Glu Arg Pro Val Val Asn Glu
 40 45 50 55
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 Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile
 60 65 70
 gac gtg gac gag aag aac cag ctt tta ata aca aac atc tgg cta aaa 595
 Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr Asn Ile Trp Leu Lys
 75 80 85

Mo5176new.txt

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Gly Val Lys Asp Leu Arg Val Pro Pro His Arg Leu Trp Lys Pro Asp	
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Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe Asp Ser Thr Tyr Pro	
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155 160 165	
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Asp Asp Gln Arg Cys Glu Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly	
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Tyr Gln Leu Asp Leu Gln Leu Gln Asp Glu Gly Gly Gly Asp Ile Ser	
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Mo5176new.txt

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cgttggtgaac ggggccgata ttgttataaa tggtaaaata cccatggcta tagcttaata 2682
aatcgttcgt taaaagttgt agttaaaca atattatattt aataaagtca tatctgggtc 2742
ttccggaacg actttttaca ataattaaat tacatatata tatcacgttt gtacttcttt 2802
ccatacagtt acagtaattc gtatgctgaa aataatatta gcttgtaaaa ttttcttctt 2862
cgaaaattta ttcaaacaga tgcgaccatc gtttcaaaca ttacatgta atatagaact 2922
cattttataa gatatacaac attttataag tacaagaagt tgtaacatga accgggtttt 2982
cgttacatag aggggtataac acaaagggtg ctacatattg acagatgcga agcacgatca 3042
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gttctaactc atcgattca tttcattcaa aaacattgta aacctctcaa ggggaaaacg 3222
tggtgtaaac agtgagagtg cgcggtgaca accgacacgc gaatgtaccc tcgcaaggct 3282
cctgtaatgt tttcctcttc cgaggtgttg ctgagagtaa tcttagacgg tccgatggaa 3342
gttgcggaac ggatatgatt acaagtcaat gtttttaagt catccgttta tttattgtta 3402
tatcttctta ccattcgcta gaggttgtgt gacgaccgg acggtgggag ccgcaaccgg 3462
cacacgcggg gttccatctt tgtattagat ggaagttgtg cggcatctct ccgtcggcaa 3522
tgggacaacc cgttggtccc aacatttggt caattgtag ggtaactct gaattgcact 3582
ttgtttatta aatataaacg aatgaaaca aaaaaaaaaa aaaaaactcg agagtacttc 3642
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<210> 4

<211> 496

<212> PRT

<213> *Heliothis virescens*

<400> 4

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Leu	Leu	Leu	Leu	Cys	Leu	Leu	Trp	Pro	Arg	Gly	Ala	Arg	Cys	Gly	Tyr
			20					25					30		
His	Glu	Lys	Arg	Leu	Leu	His	His	Leu	Leu	Asp	His	Tyr	Asn	Val	Leu
		35				40						45			
Glu	Arg	Pro	Val	Val	Asn	Glu	Ser	Asp	Pro	Leu	Gln	Leu	Ser	Phe	Gly
	50					55					60				
Leu	Thr	Leu	Met	Gln	Ile	Ile	Asp	Val	Asp	Glu	Lys	Asn	Gln	Leu	Leu
65					70					75				80	

Mo5176new.txt

Ile Thr Asn Ile Trp Leu Lys Leu Glu Trp Asn Asp Met Asn Leu Arg
 85 90 95
 Trp Asn Thr Ser Asp Phe Gly Gly Val Lys Asp Leu Arg Val Pro Pro
 100 105 110
 His Arg Leu Trp Lys Pro Asp Val Leu Met Tyr Asn Ser Ala Asp Glu
 115 120 125
 Gly Phe Asp Ser Thr Tyr Pro Thr Asn Val Val Val Arg Asn Asn Gly
 130 135 140
 Ser Cys Leu Tyr Val Pro Pro Gly Ile Phe Lys Ser Thr Cys Lys Ile
 145 150 155 160
 Asp Ile Thr Trp Phe Pro Phe Asp Asp Gln Arg Cys Glu Met Lys Phe
 165 170 175
 Gly Ser Trp Thr Tyr Asp Gly Tyr Gln Leu Asp Leu Gln Leu Gln Asp
 180 185 190
 Glu Gly Gly Gly Asp Ile Ser Ser Phe Val Thr Asn Gly Glu Trp Glu
 195 200 205
 Leu Ile Gly Val Pro Gly Lys Arg Asn Glu Ile Tyr Tyr Asn Cys Cys
 210 215 220
 Pro Glu Pro Tyr Ile Asp Ile Thr Phe Ala Val Val Ile Arg Arg Lys
 225 230 235 240
 Thr Leu Tyr Tyr Phe Phe Asn Leu Ile Val Pro Cys Val Leu Ile Ala
 245 250 255
 Ser Met Ala Leu Leu Gly Phe Thr Leu Pro Pro Asp Ser Gly Glu Lys
 260 265 270
 Leu Ser Leu Gly Val Thr Ile Leu Leu Ser Leu Thr Val Phe Leu Asn
 275 280 285
 Met Val Ala Glu Thr Met Pro Ala Thr Ser Asp Ala Val Pro Leu Leu
 290 295 300
 Gly Thr Tyr Phe Asn Cys Ile Met Phe Met Val Ala Ser Ser Val Val
 305 310 315 320
 Ser Thr Ile Leu Ile Leu Asn Tyr His His Arg His Ala Asp Thr His
 325 330 335
 Glu Met Ser Asp Trp Ile Arg Cys Val Phe Leu Tyr Trp Leu Pro Trp
 340 345 350
 Val Leu Arg Met Ser Arg Pro Gly Ser Ala Thr Thr Pro Pro Pro Ala
 355 360 365
 Arg Val Pro Pro Pro Pro Asp Leu Glu Leu Arg Glu Arg Ser Ser Lys
 370 375 380
 Ser Leu Leu Ala Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Pro
 385 390 395 400
 Gln Ala Gln Gln Pro Gln Cys Cys Arg Tyr Tyr Arg Gly Gly Glu Glu
 405 410 415

Asn Gly Ala Gly Leu Ala Ala His Ser Cys Phe Gly Val Asp Tyr Glu
 420 425 430
 Leu Ser Leu Ile Leu Lys Glu Ile Arg Val Ile Thr Asp Gln Met Arg
 435 440 445
 Lys Asp Asp Glu Asp Ala Asp Ile Ser Arg Asp Trp Lys Phe Ala Ala
 450 455 460
 Met Val Val Asp Arg Leu Cys Leu Ile Ile Phe Thr Leu Phe Thr Ile
 465 470 475 480
 Ile Ala Thr Leu Ala Val Leu Leu Ser Ala Pro His Ile Met Val Ser
 485 490 495

<210> 5
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 <212> DNA
 <213> *Heliothis virescens*

<220>
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 <222> (95)..(1597)

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 Met Ala Pro Met Leu Ala Ala
 1 5
 ttg gcg ctg ctg gct ttg ctg ccc gta tcg gag caa ggt cct cac gag 163
 Leu Ala Leu Leu Ala Leu Leu Pro Val Ser Glu Gln Gly Pro His Glu
 10 15 20
 aag aga ctc ctg aac gcg ttg ctg gcg aac tac aac acc ctg gag cga 211
 Lys Arg Leu Leu Asn Ala Leu Leu Ala Asn Tyr Asn Thr Leu Glu Arg
 25 30 35
 ccg gtg gcc aac gag agc gaa ccg cta gag gtc agg ttc ggc ttg acc 259
 Pro Val Ala Asn Glu Ser Glu Pro Leu Glu Val Arg Phe Gly Leu Thr
 40 45 50 55
 ttg cag caa atc att gac gtg gac gag aag aat caa cta ctt ata acc 307
 Leu Gln Gln Ile Ile Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr
 60 65 70
 aat ata tgg ctg tcg ttg gag tgg aat gac tac aac ctg agg tgg aac 355
 Asn Ile Trp Leu Ser Leu Glu Trp Asn Asp Tyr Asn Leu Arg Trp Asn
 75 80 85
 gac agc gag tat ggc ggg gtc aag gac ctc agg atc acg ccc aac aag 403
 Asp Ser Glu Tyr Gly Gly Val Lys Asp Leu Arg Ile Thr Pro Asn Lys
 90 95 100
 ttg tgg aag ccg gac gtc ctt atg tat aat agt gct gac gag ggt ttt 451
 Leu Trp Lys Pro Asp Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe
 105 110 115
 gac ggg acc tac cag acc aac gtg gtg gtc aga agc ggc ggc agt tgc 499
 Asp Gly Thr Tyr Gln Thr Asn Val Val Val Arg Ser Gly Gly Ser Cys

120	125	130	135	
ctg tac gtg cca cct ggc ata ttc aag agc aca tgc aag atg gac atc Leu Tyr Val Pro Pro Gly Ile Phe Lys Ser Thr Cys Lys Met Asp Ile	140	145	150	547
gcg tgg ttt ccc ttc gac gac caa cac tgt gat atg aag ttc ggt agc Ala Trp Phe Pro Phe Asp Asp Gln His Cys Asp Met Lys Phe Gly Ser	155	160	165	595
tgg aca tat gac ggc aat cag ttg gat ctg gtg cta aaa gat gag gca Trp Thr Tyr Asp Gly Asn Gln Leu Asp Leu Val Leu Lys Asp Glu Ala	170	175	180	643
ggc ggc gat cta tcg gac ttc ata aca aat ggg gag tgg tat cta ata Gly Gly Asp Leu Ser Asp Phe Ile Thr Asn Gly Glu Trp Tyr Leu Ile	185	190	195	691
gga atg cca ggc aaa aag aac aca ata aca tac gcg tgc tgc ccc gag Gly Met Pro Gly Lys Lys Asn Thr Ile Thr Tyr Ala Cys Cys Pro Glu	200	205	210	739
ccc tac gtg gac gtc acc ttc acc atc atg ata aga aga cga acc ttg Pro Tyr Val Asp Val Thr Phe Thr Ile Met Ile Arg Arg Arg Thr Leu	220	225	230	787
tac tac ttc ttc aac ctg atc gtc ccg tgc gtg ctg atc tca tcg atg Tyr Tyr Phe Phe Asn Leu Ile Val Pro Cys Val Leu Ile Ser Ser Met	235	240	245	835
gca ctc ctc ggc ttc aca ctg cca cca gac tcc gga gag aaa ctc aca Ala Leu Leu Gly Phe Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Thr	250	255	260	883
ctt gga gtc act att ctt cta tcg ctg acg gtg ttc ctc aac ctg gta Leu Gly Val Thr Ile Leu Leu Ser Leu Thr Val Phe Leu Asn Leu Val	265	270	275	931
gcc gag acc ctg cca cag gtc tcc gac gct atc ccc ctg tta ggg acg Ala Glu Thr Leu Pro Gln Val Ser Asp Ala Ile Pro Leu Leu Gly Thr	280	285	290	979
tac ttc aat tgc atc atg ttc atg gta gcg tcg tct gtg gta ctg act Tyr Phe Asn Cys Ile Met Phe Met Val Ala Ser Ser Val Val Leu Thr	300	305	310	1027
gtg gtg gta ctc aat tac cac cat cga aca gct gat ata cat gaa atg Val Val Val Leu Asn Tyr His His Arg Thr Ala Asp Ile His Glu Met	315	320	325	1075
cca cag tgg ata aaa tca gta ttc cta caa tgg ttg cca tgg ata ctg Pro Gln Trp Ile Lys Ser Val Phe Leu Gln Trp Leu Pro Trp Ile Leu	330	335	340	1123
cga atg tcg agg cca ggg aag aag atc acc agg aag act ata atg atg Arg Met Ser Arg Pro Gly Lys Lys Ile Thr Arg Lys Thr Ile Met Met	345	350	355	1171
aac acg agg atg agg gag ctg gaa ctg aag gag agg tcg tcg aag tcc Asn Thr Arg Met Arg Glu Leu Glu Leu Lys Glu Arg Ser Ser Lys Ser	360	365	370	1219
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Mo5176new.txt

Leu Leu Ala Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Gly Pro
 380 385 390
 ccg cct cct aac agt act gcc tcg acc ggg aat ttg gga cct ggg tgc 1315
 Pro Pro Pro Asn Ser Thr Ala Ser Thr Gly Asn Leu Gly Pro Gly Cys
 395 400 405
 tca ata ttc cgc acg gat ttc cgt cgg tcg ttc gtc cgt ccg tcc acg 1363
 Ser Ile Phe Arg Thr Asp Phe Arg Arg Ser Phe Val Arg Pro Ser Thr
 410 415 420
 atg gaa gac gtg ggc ggc ggg ctg ggt agc cac cat cgc gag ctg cac 1411
 Met Glu Asp Val Gly Gly Gly Leu Gly Ser His His Arg Glu Leu His
 425 430 435
 ctc ata ctg aga gag ctg cag ttc atc acg gcc agg atg aag aag gct 1459
 Leu Ile Leu Arg Glu Leu Gln Phe Ile Thr Ala Arg Met Lys Lys Ala
 440 445 450 455
 gat gag gaa gcc gag ctg atc agc gac tgg aag ttt gct gcg atg gtt 1507
 Asp Glu Glu Ala Glu Leu Ile Ser Asp Trp Lys Phe Ala Ala Met Val
 460 465 470
 gtt gat agg ttt tgc ctg ttc gtg ttc aca ctt ttc aca atc atc gcg 1555
 Val Asp Arg Phe Cys Leu Phe Val Phe Thr Leu Phe Thr Ile Ile Ala
 475 480 485
 aca gta gct gtc ctg tta tcg gca ccg cat atc atc gtg caa 1597
 Thr Val Ala Val Leu Leu Ser Ala Pro His Ile Ile Val Gln
 490 495 500
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 ccgattttgta attataattg ataatgtaat taaattaaat acgtggttga aacgcacacg 1717
 tctccataac aaagtcttaa gacattaaat tatgataaat ttacatattg tagttaagtc 1777
 gagtgttgat ggaaatttta gccggcgcaa ggagtttcgt gaaggctctgt atatattttt 1837
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 gtttgtttct tcgatggcag gtgcacttca gttcaggctg aaatttccat taacatttat 1957
 ttaaacaat gtgatgttga ctaggatgtt atacagataa atgttgacgt gtataatttg 2017
 ttaaaataaa caatattaat tactattact aaacgatatt ataaacgaag tactaacgag 2077
 gggtacttta atgggaagaa cgctaagctg gcacagagtt gcattaattt gaaaaaagaa 2137
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Mo5176new.txt

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<210> 6

<211> 501

<212> PRT

<213> *Heliothis virescens*

<400> 6

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 35 40 45
 Glu Val Arg Phe Gly Leu Thr Leu Gln Gln Ile Ile Asp Val Asp Glu
 50 55 60
 Lys Asn Gln Leu Leu Ile Thr Asn Ile Trp Leu Ser Leu Glu Trp Asn
 65 70 75 80
 Asp Tyr Asn Leu Arg Trp Asn Asp Ser Glu Tyr Gly Gly Val Lys Asp
 85 90 95
 Leu Arg Ile Thr Pro Asn Lys Leu Trp Lys Pro Asp Val Leu Met Tyr
 100 105 110
 Asn Ser Ala Asp Glu Gly Phe Asp Gly Thr Tyr Gln Thr Asn Val Val
 115 120 125
 Val Arg Ser Gly Gly Ser Cys Leu Tyr Val Pro Pro Gly Ile Phe Lys
 130 135 140
 Ser Thr Cys Lys Met Asp Ile Ala Trp Phe Pro Phe Asp Asp Gln His
 145 150 155 160
 Cys Asp Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Asn Gln Leu Asp
 165 170 175
 Leu Val Leu Lys Asp Glu Ala Gly Gly Asp Leu Ser Asp Phe Ile Thr
 180 185 190

Asn Gly Glu Trp Tyr Leu Ile Gly Met Pro Gly Lys Lys Asn Thr Ile
 195 200 205
 Thr Tyr Ala Cys Cys Pro Glu Pro Tyr Val Asp Val Thr Phe Thr Ile
 210 215 220
 Met Ile Arg Arg Arg Thr Leu Tyr Tyr Phe Phe Asn Leu Ile Val Pro
 225 230 235 240
 Cys Val Leu Ile Ser Ser Met Ala Leu Leu Gly Phe Thr Leu Pro Pro
 245 250 255
 Asp Ser Gly Glu Lys Leu Thr Leu Gly Val Thr Ile Leu Leu Ser Leu
 260 265 270
 Thr Val Phe Leu Asn Leu Val Ala Glu Thr Leu Pro Gln Val Ser Asp
 275 280 285
 Ala Ile Pro Leu Leu Gly Thr Tyr Phe Asn Cys Ile Met Phe Met Val
 290 295 300
 Ala Ser Ser Val Val Leu Thr Val Val Val Leu Asn Tyr His His Arg
 305 310 315 320
 Thr Ala Asp Ile His Glu Met Pro Gln Trp Ile Lys Ser Val Phe Leu
 325 330 335
 Gln Trp Leu Pro Trp Ile Leu Arg Met Ser Arg Pro Gly Lys Lys Ile
 340 345 350
 Thr Arg Lys Thr Ile Met Met Asn Thr Arg Met Arg Glu Leu Glu Leu
 355 360 365
 Lys Glu Arg Ser Ser Lys Ser Leu Leu Ala Asn Val Leu Asp Ile Asp
 370 375 380
 Asp Asp Phe Arg His Gly Pro Pro Pro Pro Asn Ser Thr Ala Ser Thr
 385 390 395 400
 Gly Asn Leu Gly Pro Gly Cys Ser Ile Phe Arg Thr Asp Phe Arg Arg
 405 410 415
 Ser Phe Val Arg Pro Ser Thr Met Glu Asp Val Gly Gly Gly Leu Gly
 420 425 430
 Ser His His Arg Glu Leu His Leu Ile Leu Arg Glu Leu Gln Phe Ile
 435 440 445
 Thr Ala Arg Met Lys Lys Ala Asp Glu Glu Ala Glu Leu Ile Ser Asp
 450 455 460
 Trp Lys Phe Ala Ala Met Val Val Asp Arg Phe Cys Leu Phe Val Phe
 465 470 475 480
 Thr Leu Phe Thr Ile Ile Ala Thr Val Ala Val Leu Leu Ser Ala Pro
 485 490 495
 His Ile Ile Val Gln
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 <213> Artificial Sequence

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 <221> modified_base
 <222> (6)
 <223> i

<400> 7
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20

<210> 8
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> modified_base
 <222> (9)
 <223> i

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20

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32

<210> 10
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<220>
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27

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<220>
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<220>
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<210> 13
<211> 27
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<400> 13
gcaagcgccg ctatggcccc tatgttg 27

<210> 14
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